

SEQUENCE LISTING

```
RECEIVED
<110> Bonnert, Timothy Peter
<120> HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR
                                                      JUN 1 9 2002
<130> T1481
                                                  TECH CENTER 1600/2900
<140> 09/445,614
<141> 1999-12-08
<150> 9827016.8
<151> 1998-12-08
<160> 19
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 2469
<212> DNA
<213> Homo sapiens
<400> 1
                                                                      60
cacgaggccg acgcgcagct gggaggaaga caggaccctt gacatctcca tctgcacaga
                                                                     120
ggtcctggct ggaccgagca gcctcctcct cctaggatga cctcaccctc cagctctcca
                                                                     180
gttttcaggt tggagacatt agatggaggc caagaagatg gctctgaggc ggacagagga
                                                                     240
aagctggatt ttgggagcgg gctgcctccc atggagtcac agttccaggg cgaggaccgg
                                                                     300
aaattcgccc ctcagataag agtcaacctc aactaccgaa agggaacagg tgccagtcag
                                                                     360
ccqqatccaa accqatttqa ccqaqatcqq ctcttcaatq cggtctcccg gggtgtcccc
gaggatctgg ctggacttcc agagtacctg agcaagacca gcaagtacct caccgactcg
                                                                     420
qaatacacaq aqqqctccac aggtaagacg tgcctgatga aggctgtgct gaaccttaag
                                                                     480
                                                                     540
gacggagtca atgcctgcat tctgccactg ctgcagatcg acagggactc tggcaatcct
cagcccctgg taaatgccca gtgcacagat gactattacc gaggccacag cgctctgcac
                                                                     600
atcgccattg agaagaggag tctgcagtgt gtgaagctcc tggtggagaa tggggccaat
                                                                     660
                                                                     720
gtgcatgccc gggcctgcgg ccgcttcttc cagaagggcc aagggacttg cttttatttc
                                                                     780
ggtgagctac ccctctcttt ggccgcttgc accaagcagt gggatgtggt aagctacctc
ctggagaacc cacaccagcc cgccagcctg caggccactg actcccaggg caacacagtc
                                                                     840
ctgcatgccc tagtgatgat ctcggacaac tcagctgaga acattgcact ggtgaccagc
                                                                     900
atgtatgatg ggctcctcca agctggggcc cgcctctgcc ctaccgtgca gcttgaggac
                                                                     960
atccgcaacc tgcaggatct cacgcctctg aagctggccg ccaaggaggg caagatcgag
                                                                    1020
attttcaggc acatcctgca gcgggagttt tcaggactga gccacctttc ccgaaagttc
                                                                    1080
                                                                    1140
accgagtggt gctatgggcc tgtccgggtg tcgctgtatg acctggcttc tgtggacagc
                                                                    1200
tgtgaggaga actcagtgct ggagatcatt gcctttcatt gcaagagccc gcaccgacac
                                                                    1260
cgaatggtcg ttttggagcc cctgaacaaa ctgctgcagg cgaaatggga tctgctcatc
                                                                    1320
cccaagttct tcttaaactt cctgtgtaat ctgatctaca tgttcatctt caccgctgtt
                                                                    1380
gcctaccatc agcctaccct gaagaagcag gccgccctc acctgaaagc ggaggttgga
aactccatgc tgctgacggg ccacatcctt atcctgctag gggggatcta cctcctcgtg
                                                                    1440
ggccagctgt ggtacttctg gcggcgccac gtgttcatct ggatctcgtt catagacagc
                                                                    1500
                                                                    1560
tactttgaaa tcctcttcct gttccaggcc ctgctcacag tggtgtccca ggtgctgtgt
                                                                    1620
1680
aacctgcttt actatacacg tggcttccag cacacaggca tctacagtgt catgatccag
                                                                    1740
aaggtcatcc tgcgggacct gctgcgcttc cttctgatct acttagtctt ccttttcggc
                                                                    1800
ttcgctgtag ccctggtgag cctgagccag gaggcttggc gccccgaagc tcctacaggc
                                                                    1860
```

cccaatgcca cagagtcagt gcagcccatg gagggacagg aggacgaggg caacggggcc

```
cagtacaggg gtatcctgga agcctccttg gagctcttca aattcaccat cggcatgggc
gagctggcct tccaggagca gctgcacttc cgcggcatgg tgctgctgct gctgctggcc
tacgtgctgc tcacctacat cctgctgctc aacatgctca tcgccctcat gagcgagacc
gtcaacagtg tcgccactga cagctggagc atctggaagc tgcagaaagc catctctgtc
ctggagatgg agaatggcta ttggtggtgc aggaagaagc agcgggcagg tgtgatgctg
accepttegca ctaagccaga tegcagccce gateagcect egtecttcae egtegageag
gtgaactggg cttcatggga gcagacgctg cctacgctgt gtgaggaccc gtcaggggca
ggtgtccctc gaactctcga gaaccctgtc ctggcttccc ctcccaagga ggatgaggat
ggtgcctctg aggaaaacta tgtgcccgtc cagctcctcc agtccaactg atggcccaga
tqcaqcaqqa qqccaqaqqa caqaqcaqaq gatctttcca accacatctg ctggctctgg
ggtcccagt
<210> 2
<211> 764
<212> PRT
<213> Homo sapiens
<400> 2
Met Thr Ser Pro Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
                                    1.0
Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
            20
                                25
Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
                            40
Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
                        55
                                            60
Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
                    70
                                        75
Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
                                    90
Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
                                105
Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
                            120
Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp
                                            140
    130
                        135
Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr
                    150
                                        155
Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu
                                    170
                165
Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg
            180
                                185
Ala Cys Gly Arg Phe Phe Gln Lys Gly Gln Gly Thr Cys Phe Tyr Phe
                                                205
                            200
Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val
                        215
                                            220
Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala
                                        235
                    230
Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser
                245
                                    250
Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly
                                                     270
                                265
Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp
```

1980

2040

2100 2160

2220

2280 2340

2400

2460

2469

CI Cont

275

280

.∙ T≀481

Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Gly Gly Ile Tyr Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr

Cont

```
Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn
               725
                                    730
Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu
                                745
Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn
       755
                            760
<210> 3
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 3
                                                                        51
tgttaccaat ctgaagtggg agcggccgcc tcatttttt tttttttt t
<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR Primer
<400> 4
                                                                        21
caggcccggg catgcacatt g
<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR Primer
<400> 5
                                                                        21
ccagggcgag gaccggaaat t
<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR Primer
<400> 6
                                                                        21
gacagctgga gcatctggaa g
<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence
```

C'

<220> <223> PCR Primer	
<400> 7 gacagctgga gcatctggaa g	21
<210> 8 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 8 cttccagatg ctccagctgt c	21
<210> 9 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 9 tttgccacca gaattcactg g	21
<210> 10 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 10 ctctctttgg ccgcttgcac c	21
<210> 11 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 11 ccagcactga gttctcctca c	21
<210> 12 <211> 21 <212> DNA <213> Artificial Seguence	

<220> <223> PCR Primer	
<400> 12 gccctaccgt gcagcttgag g	21
<210> 13 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 13 tgccccacga ggaggtagat c	21
<210> 14 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 14 atggcgatgt gcagagcgct g	21
<210> 15 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 15 agagtcaacc tcaaactacc g	21
<210> 16 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 16 gagettetee etgeggteaa g	21
<210> 17 <211> 21 <212> DNA <213> Artificial Sequence	

Cont.

<220> <223> PCR Primer	
<400> 17 aaggctgctg aaaaagcact g	21
<210> 18 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 18 gctgggctgg ctgaacctgc	20
<210> 19 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> PCR Primer	
<400> 19 gagggcaatg agcatgttg	19